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Research Article

Molecular Confirmation and Morphological Characterization of *Aculops lycopersici* (Tryon, 1917) (Acari: Eriophyidae) on Tomato Seedlings in Central Iraq

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ABSTRACT

The tomato russet mite, *Aculops lycopersici* (Tryon, 1917) (Acari: Eriophyidae), is a major global pest of tomato causing damage to both seedlings and mature plants. In Iraq, its identification has previously relied mainly on morphological observations, which may lead to misidentification due to closely related species. Therefore, this study aimed to confirm *A. lycopersici* infesting tomato in Baghdad using morphological and molecular approaches and to assess its seasonal abundance and associated symptoms under field conditions. Morphological examination revealed diagnostic features typical of *A. lycopersici*, including a fusiform body, distinct prodorsal shield pattern, numerous opisthosomal annuli, and a four-rayed empodium. Molecular identification using mitochondrial cytochrome c oxidase subunit I (COI) gene amplification produced a clear band of approximately 650 bp. Sequence analysis showed 98-100% identity with authenticated *A. lycopersici* sequences available in GenBank, and phylogenetic analysis clustered the Iraqi isolates within a well-supported *A. lycopersici* clade, confirming the species identity. A total of 200 tomato leaf samples were examined, of which 95.5% were positive for the mite, indicating its widespread occurrence. Population densities varied seasonally, with peak abundance recorded in mid-May (45 mites per leaf), while lower densities occurred during September and October. Infested plants exhibited characteristic symptoms including leaf bronzing, upward curling, and stem discoloration. Generally, the combined morphological and molecular evidence provides the first confirmed molecular record of *A. lycopersici* in Iraq and highlights its high prevalence and seasonal dynamics in tomato fields, emphasizing the need for effective monitoring and management strategies.

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Introduction

The fruit of tomato (*Solanum lycopersicum L.)* is one of the most important vegetable crops in the world (El-Halawany, 2012). It is one of the leading constituents of protected and open-field growing systems especially in the tropics and subtropics. The globe has recently produced more than 180 million tons of this crop, which is especially important for its nutritive and commercial properties (FAOSTAT, 2023). In Iraq, tomato is widely cultivated and is an important source of farmers' income, especially in the central and southern regions of the country.

Among arthropod pests associated with tomatoes, the eriophyid mites (Acari: Eriophyidae) are of significant

importance. These mites have minute size, reproduce rapidly and are associated with huge physiological injurious activities. Having devastating potential, one of the most destructive of eriophyid mites associated with tomato crop worldwide is the tomato rust mite, *Aculops lycopersici* (Tryon, 1917) which has been recorded from most of the tropical and temperate regions of Europe, the Americas, Asia and the Middle East (Jeppson et al., 1975; Lindquist et al., 1996; CABI, 2021). The mite has also been reported in neighboring countries such as Yemen (Estay, 2017; Negm and Alsharhi, 2018).

The infestation by *A. lycopersici* normally starts on the lower surfaces of the leaves and moves up as the population increases (Sumer et al., 2008). They suck away metabolically important substances from the cells of the plant causing the leaf to turn bronze. The infected leaves curl upward, the stems roughen, the skin of the fruits appears bumpy, and can even give rise to a very serious drop in yield of the crop. The pest is mostly injurious when the weather is warm and dry, completes its life cycle rapidly and attains a population density that can cause serious injuries and huge losses (Childers and Rodrigues, 2005; Vacante, 2010).

In Iraq, eriophyid mites associated with tomato have been reported under the synonymous names of *Vasates lycopersici* (Al-Ali, 1977) and *Aceria lycopersici* (Al-Mallah, 2009) based only on their morphology. Nonetheless, many species within the family Eriophyidae are morphologically similar; therefore, reliance only on physical characters can lead to misidentification. Molecular characterization, particularly DNA-based analysis, is necessary to accurately distinguish closely related species.

Mitochondrial cytochrome c oxidase subunit I (COI) sequencing has become a widely used and reliable method for identifying species in mites and other arthropods. Molecular confirmation refines species identification, places species in the family tree of life, and provides trusted reference sequences for future tracking.

For this reason, the present study was carried out with the aim to (1) characterize the physical attributes of eriophyid mites on tomato seedlings in central Iraq, (2) certify their species using DNA barcoding based on COI, and (3) record their seasonal fluctuations in local greenhouses. The study, therefore, provided the first molecularly validated record of *Aculops lycopersici* from Iraq and the baseline data for future IPM initiatives.

Materials and Methods

Morphological diagnosis of eriophyid mites on tomato seedlings

Sampling and slide preparation

Eriophyid mite specimens were obtained from diseased tomato seedlings during regular fortnightly inspections between 1 October 2024 and 15 April 2025 from the experimental fields of the College of Agricultural Engineering Sciences, University of Baghdad. Infested leaves were examined under a stereomicroscope (BioLab BLS120) at 80×. Individual mites were removed from the underside and the upper side of leaves using fine eyelash brush on a dissecting needle and mounted on glass slides in groups of 15-20 per sampling date to predict frequency and density of the species. Each slide was labelled with a code showing the date and location of sampling. Once mounting was complete, all slides were allowed to dry completely, prior to examination for diagnostic taxonomic information under a compound light microscope. Thirty slides were selected for use in diagnostics from the overall data set, showcasing representative specimens in good morphological condition.

Preparation of Keifer's mounting solutions

Specimens were mounted using modified Keifer's solutions following the protocols described by Amrine and Manson (1996) and Al-Jubouri (2010). The compositions of the three solutions were as follows:

Solution I

1. Gum Arabic (1 g)
2. Resorcinol (3 g)
3. Potassium iodide (0.2 g)
4. Iodine crystals (0.20–0.32 g)

These components were finely ground in a ceramic mortar. Subsequently, 10 cm^3 of 85% lactic acid and several drops of hydrochloric acid were added, and the mixture was thoroughly homogenized.

Solution II

1. Sucrose (1 g)
2. Chloral hydrate (8 g)
3. Potassium iodide (0.2 g)
4. Iodine crystals (0.32 g)

The dry components were ground and transferred to a test tube, followed by the addition of approximately 30 drops of ½ normal formaldehyde solution. The mixture was shaken until completely dissolved.

Solution III

1. Gum Arabic (0.5 g)
2. Sucrose (0.5 g)

3. Chloral hydrate (7 g)
4. Potassium iodide (0.2 g)

The components were ground and mixed with approximately 18 drops of ¼ normal formaldehyde solution until fully homogenized.

Mounting procedure

A small drop of solution I was transferred to the surface of a Petri dish, and individual mite specimens were moved into the solution on the surface of the dish by brushing them off a pin or other transfer device, using the stereomicroscope. The dish was then warmed in the water bath (≈ 5 min) to accelerate clarification. Specimens were then transferred to a drop of Solution II for 30-40 min to remove excess resorcinol and render them relatively transparent. Finally, mites were transferred to a drop of Solution III on a clean glass slide and covered with a coverslip. The slides were dried overnight in a laboratory oven maintained at > 40°C. After total desiccation (which was not fully achieved until after several weeks), specimens were examined at 400× magnification using a compound microscope, viewed dorsally, ventrally and in lateral aspect, to note diagnostic morphological characters.

Species identification and frequency determination

After preliminary identification, representative individuals were examined and confirmed by an expert in acarology at the Plant Protection Department, University of Baghdad. Two hundred specimens were then examined for species composition and seasonal frequency on tomato seedlings. The chemical components used in the preparation of Keifer's mounting solutions are listed in Table 1.

Table 1. Chemical compounds used in the preparation of Keifer's mounting solutions.

Chemical name	Chemical formula	Manufacturer
Chloral hydrate	$C_2H_3Cl_3O_2$	BDH
Formaldehyde	HCHO	Scharlau Chemie
Gum Arabic	—	Thomas Baker
Hydrochloric acid	HCl	Gainland Chemical
Iodine	I_2	Gainland Chemical
Lactic acid	$C_3H_6O_3$	Gainland Chemical
Potassium iodide	KI	AppliChem GmbH
Resorcinol	$C_6H_6O_2$	Baha Durgarh
Sucrose	$C_{12}H_{22}O_{11}$	Thomas Baker

Chemical information was verified according to manufacturer specifications and standard laboratory references (Sigma-Aldrich, 2000-2001; Al-Jubouri, 2010).

Molecular Identification of *Aculops lycopersici*

DNA extraction

Molecular analyses were undertaken at Jisr Al-Maseeb and Macrogen Inc. (South Korea). Genomic DNA was extracted directly from eriophyid mite specimen(s) scraped from infested tomato leaf material. About 10-20 adult mite(s) were pooled (for each extraction), into a 1.5 ml sterile microcentrifuge tube to achieve an adequate DNA yield and specimens were briefly frozen in liquid nitrogen and homogenized using a sterile micro pestle.

DNA was extracted using a commercial genomic DNA extraction kit (Geneaid Biotech Ltd., Taiwan) according to the manufacturer's protocol with minor modifications. The extraction procedure included the following steps:

1. Portion of homogenized lysate tissues was mixed with 200 µl of lysis buffer (GST buffer) and 20 µl of Proteinase K (20 mg/ml).
2. The samples were briefly vortexed and incubated overnight at 60°C (1-3 h until tissue completely lysed, the tubes were gently inverted intermittently after every hour).
3. After incubation, samples were centrifuged at 14,000-16,000 rpm for 2 min. The supernatant was transferred to a new micro-centrifuge tube.
4. To this, 200 µl of GSB binding buffer was added and mixed thoroughly followed by the addition of 200 µl of absolute ethanol. The sample was then briefly vortexed to ensure binding conditions.
5. The entire lysate was transferred to a spin column placed in a 2 ml collection tube and centrifuged for 1 min at 14,000-16,000 rpm. The flow-through was then discarded.
6. The column was washed with 400 µl of W1 buffer and centrifuged for 30 sec, and then washed with 600 µl of wash buffer and centrifuged for 3 min to completely dry the membrane.
7. The DNA was eluted by adding 100 µl of preheated elution buffer (60°C) directly to the center of the column membrane, incubated for 1 min, and centrifuged at 14,000 rpm for 5 min.

Extracted DNA samples were stored at -20°C until PCR amplification.

DNA quantification and quality assessment

DNA concentration and purity were measured using a Thermo Scientific UV-Vis spectrophotometer (USA). Absorbance was measured at 260 nm and 280 nm respectively, to estimate both concentration and level of

protein contamination. As an indicator of purity, A260/A280 ratios between 1.7 and 2.0 were considered acceptable and suitable for use in PCR amplification. Unacceptable samples were diluted or concentrated as necessary to obtain approximately 50-100 ng per reaction.

Polymerase chain reaction (PCR)

An approximately 700 bp fragment of the mitochondrial cytochrome c oxidase subunit I (COI) gene was amplified using the universal primer pair LCO1490 (5′– GGTCAACAAATCATAAAGATATTGG– 3′) and HCO2198 (5′– TAAACTTCAGGGTGACCAAAAAATCA– 3′), following the protocol outlined by Folmer et al. (1994).

Primers were synthesized by Macrogen Inc. (South Korea) at a concentration of 10 pmol/µL. PCR amplification was performed in a total reaction volume of 50 µl containing 25 µl of 2× Taq DNA Polymerase Master Mix (Ampligon, Denmark), 2.5 µl of each primer, 50-100 ng of template DNA and nuclease-free water to obtain the final volume of 50 µl. The COI gene region was selected because it provides sufficient interspecific variability while remaining relatively conserved within species, making it a reliable marker for species-level identification in arthropods (Folmer et al., 1994). The primers used for amplification of the COI gene are presented in Table 2.

Cycler Techne TC-3000× Thermal cycler (UK) was performed according to the cycling condition detailed in Table 3.

Table 2. Primers used for amplification of the mitochondrial COI gene region.

Primer name	Nucleotide sequence (5′-3′)	T (°C)*	Expected fragment size (bp)	Reference
LCO1490	GGTCAACAAATCATAAAGATATTGG	48-50	~658	Folmer et al., 1994
HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	50-52	~658	Folmer et al., 1994

*Tm values may vary slightly depending on reaction conditions and calculation method.

Table 3. Thermal cycling conditions used for PCR amplification of the mitochondrial COI gene region.

Step	T (°C)	Time	Cycles
Initial denaturation	94	4 min	1
Denaturation	94	30 sec	35
Annealing	57	1 min	35
Extension	72	1 min	35
Final extension	72	10 min	1
Hold	4	∞	-

Primers: LCO1490 / HCO2198 (Folmer et al., 1994).

Agarose gel electrophoresis

PCR products were analyzed by electrophoresis on 2% agarose gel in 1× TAE buffer at 95 V for approximately 45-60 min using a Cleaver Scientific MultiSUB electrophoresis unit (EV222, UK). A 100 bp DNA ladder (Promega, USA) was used as molecular size marker. Gels were stained with 1× DNA fluorescent dye (Promega, USA) and visualized by UV illumination using a Cleaver UVT254/312 gel documentation system (UK). The presence of one clear band of expected size (~658 bp) confirmed successful amplification of the COI gene fragment.

DNA sequencing

PCR products showing clear single bands were purified and sent to Macrogen Inc. (South Korea) for bidirectional Sanger sequencing using the same primer pair employed for amplification.

Molecular identification and sequence analysis

The raw chromatograms were viewed and edited using BioEdit Sequence Alignment Editor version 7.1. The ends of the data were trimmed before analysis. Consensus sequences were formed from forward and reverse reads. The envisaged edited sequences were then compared against existing reference sequences on the National Center for Biotechnology Information (NCBI) database using the BLASTn algorithm (Zhang et al., 2000). Species were identified based on percentage identity, query coverage and maximum alignment score. Sequences showing ≥ 98% identity with authenticated *A. lycopersici* sequences in GenBank were considered conspecific.

Multiple sequence alignment was conducted by employing the Clustal W tool accessible from MEGA version 7 (Kumar et al., 2016). Neighbor-joining trees were constructed with Kimura 2-parameter method as the distance metric. The confidence in the inferred trees was evaluated with bootstrap analysis, using 1000 replications. All validated sequences generated in this study were submitted to GenBank, and accession numbers were obtained accordingly.

Statistical analysis

Seasonal mite population density data of *A. lycopersici* were subjected to one-way analysis of variance (ANOVA) according to the sampling dates. Mean density of the mite per leaf was examined for each sampling interval

and expressed as mean ± SE. In cases where large differences were observed, means were separated by the LSD test at P ≤ 0.05 and all statistical analyses were performed using SPSS (Version 26.0; IBM Corp., USA).

Results and Discussion

Morphological and molecular confirmation of *A. lycopersici*

The morphological-molecular analysis indicated that the eriophyid mite associated with infested tomato seedlings in Baghdad is *A. lycopersici* (Tryon, 1917). The morphology showed diagnostic characters consistent those given in previous descriptions of *A. lycopersici* (spindle shape body, clear prodorsal shield pattern, transverse genital opening in females with a cover flap, characteristically shaped opisthosomal annuli) (Jeppson et al. 1975; Lindquist et al.1996; Krantz and Walter 2009) available in the literature. The eriophyid mites on tomato in Iraq were previously reported either as *Vasates lycopersici*, *Aceria lycopersici* or other synonymous names (Al-Ali 1977; Al-Mallah 2009), and the records indirectly refer to this species. However, these records were based solely on morphological evidence. This paper provided the first report of *A. lycopersici* in Iraq based on molecular identification. Sequencing of the mitochondrial COI gene displayed 98-100% identity with authenticated *A. lycopersici* sequences present in GenBank. Phylogenetic analysis grouped Iraqi isolates into the well-supported *A. lycopersici* clade, reaffirming its identity.

Seasonal abundance

A total of 200 leaf samples were examined and out of which 191 (95.5%) were found positive for *A. lycopersici* (Table 4). The mite was found in most of the growing season. Population densities varied between the sampling dates. This pattern is consistent with previous studies reporting seasonal fluctuations of eriophyid mites on tomato (Abd-Alkawy et al., 2021).Highest mean density was observed in mid-May (45 mites per leaf), followed by late May (26 mites per leaf) and mid-June (21 mites per leaf). Significantly lower densities were found during September and October, with densities ranging between 8 and 13 mites per leaf. The high positive rate (95.5%) indicates that this species is well established under farm conditions.

Symptomatology and ecological observations

Infested tomato seedlings also showed characteristic symptoms of bronzing of the leaves, upward curling, and discoloration of the stem. These symptoms are similar to feeding damage described by *A. lycopersici* (Gerson et al., 2003; Krantz and Walter, 2009). Mites were found mainly on the lower surface of the leaves. Their extremely small body size (< 0.2 mm) and presence of leaf trichomes might effectively protect them from predators and direct radiation from the sun (Jeppson et al., 1975; Gerson et al., 2003). Populations peaked in warmer months, which were also found by Childers and Rodrigues (2005) who recorded increased abundances of *A. lycopersici* under relatively warm drier conditions. This species has a cyst-producing life cycle and a high level of reproduction in protected cultivation systems (Lindquist et al., 1996; Vacante, 2010; Pfaf et al., 2024).

Table 4. Seasonal abundance of *A. lycopersici* on tomato seedling leaves in Al-Jadriya, Baghdad (01/10/2024 to 15/04/2025).

Sampling date	No. of Leaves examined	Mean mites per leaf
01/10/2024	15	13
15/10/2024	15	8
01/11/2024	20	17
15/11/2024	16	18
01/12/2024	15	12
15/12/2024	14	12
01/01/2025	15	11
15/01/2025	10	11
01/02/2025	18	15
15/02/2025	20	17
01/03/2025	15	14
15/03/2025	15	13
15/04/2025	17	16
Total leaves examined	200	-
Positive samples (n)	191	-
Infestation rate (%)	-	95.5

General description and morphological diagnosis of *A. lycopersici*

The examined specimens were identified as *A. lycopersici* (Tryon, 1917) (Acari: Eriophyidae) based on diagnostic morphological characters. Adult females were fusiform, pale yellow to light brown when alive; 150-180 µm long; 45-55 µm wide, males were similar but smaller (132-163 µm long; 42-51 µm wide) (Figure 1).

The prodorsal shield was semi-triangular, approximately 25-30 µm long in females, having a short and broad lobe drooping anteriorly; ornamentation of the shield represented a distinct median line extended posteriorly and lateral cell-like figures formed by transverse and branched lines along both posterior margins. There were

three pairs of anterior setae: a short anterior pair located adjacent to the anterior margin and two pairs that were longer laterally, elongated anterolaterally.



Figure 1. Seasonal variation in the mean number of *A. lycopersici* per tomato leaf in Al-Jadriya, Baghdad, from 01 October 2024 to 15 April 2025.

The gnathostome was directed downward, with stylet-like chelicerae adapted for piercing and sucking. Eyes and Peritreme were absent, consistent with typical eriophyid morphology. Opisthosoma with numerous dorsal annuli (ca. 60) bearing micro tubercles giving a beaded appearance; dorsal setae short; coxal region with characteristic arrangement of setae of the genus.

Employing four rays, the empodium (feather claw) was a character distinguishing it to the specific as *A. lycopersici*. The female genital opening was transverse, situated behind the second pair of legs, protected by a genital cover flap ornamented with about ten longitudinal ridges. Males lacked the genital cover flap.

These morphological characters are consistent with the normal taxonomic outline of *A. lycopersici* given in the general works on acarology (Jeppson et al., 1975; Lindquist et al., 1996; Krantz and Walter, 2009) and with reports on more recent regional collections (Al-Azzazy and Alhewairini, 2018). The morphological features of *A. lycopersici* are illustrated in Figure 2.

Molecular diagnosis of *A. lycopersici* using PCR

The products were then subjected to agarose gel electrophoresis, which ultimately revealed one clear band, approximate size of 650 bp, corresponding to the size of the mitochondrial cytochrome c oxidase subunit I (COI) gene expected. The absence of additional/noise bands supported successful and specific amplification of the desired region (Figure 3).

Regular sequencing of the amplified fragment followed by a BLASTn search demonstrated similar matches (98%-100% identity) with authenticated *A. lycopersici* sequences in the GenBank database (Table 5). The sequence was deposited in GenBank with the accession number PX426844.1.

The molecular results are fully consistent with the morphological diagnosis and provide independent confirmation of the taxonomic identity of the examined specimens as *A. lycopersici*.



Figure 2. (A) Adult female of *A. lycopersici* viewed dorsally. This mite features a prodorsal shield and rigidly annulated opisthosoma, (B) Seen laterally. The entire body is rigidly annulated, with the head gear being feebly ribbed and semi-transparent, (C) Ventrally, it bears a transverse genital opening as well as a 2-segmented genital cover flap, (D) Feather claw (empodium) associated with the anterior legs and (E) Dorsal view and ventral view showing micro tubercles on the annuli.

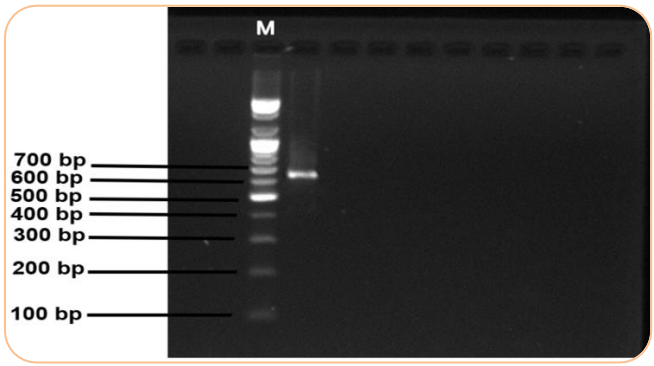


Figure 3. Agarose gel electrophoresis of PCR-amplified mitochondrial COI gene fragment of *A. lycopersici*. Lane M: 100 bp DNA ladder (molecular size marker). Lane 1: PCR product of the examined *A. lycopersici* isolate showing a single band of approximately 650 bp.

Sequence comparison and genetic homogeneity

Using BLASTn, the obtained mitochondrial COI sequence showed high similarity (98 to 100% identity) to authenticated *A. lycopersici* sequences in GenBank. The final edited sequence after trimming of the low-quality ends was 531 bp. Previous molecular studies have revealed little evidence for intraspecific variation in *A. lycopersici* globally, and COI sequences are generally > 98% identical among distant geographical isolates (Arribas et al., 2020; Abeynayake et al., 2021; Duarte et al., 2023). Levels of sequence identity are regarded as compelling molecular evidence for species confirmation in eriophyid mites.

In their phylogenetic analysis, sequences from Iraq clustered in a well-supported clade containing *A. lycopersici* sequences from Europe and South America (Chavera et al., 2015), indicating low genetic divergence and is consistent with the reported global genetic uniformity of this species. Sequence identity comparisons with reference isolates are shown in Table 6.

Phylogenetic analysis

Phylogenetic analysis revealed that Iraqi isolates were clearly rooted in the strongly supported *A. lycopersici* clade based on mitochondrial COI sequences (Figure 4). The sequences obtained were closely grouped with authenticated reference sequences accessed from GenBank, creating a monophyletic lineage separate from other related eriophyids. Bootstrap support values indicated high statistical support for the placement of samples studied within each lineage. No significant divergence was observed in Iraqi isolates in comparison to internationally derived reference sequences, enhancing the species identification basis. This provided independent molecular evidence that confirmed the studied specimens indeed belong to the genus *Aculops* (as evident in the morphological diagnosis) and to *A. lycopersici*.

Table 5. GenBank accession number and sequence characteristics of *Aculops lycopersici* isolate obtained in this study.

Species	Isolate / Voucher ID	GenBank accession number	Country	Sequence length (bp)
A. lycopersici	Iraqi isolate (2025)	PX426844.1	Iraq (This study)	531

Sequence length reflects trimming of low-quality ends prior to alignment and phylogenetic analysis.

Table 6. Percentage identity of Iraqi *A. lycopersici* isolates compared with selected GenBank reference sequences (COI gene).

Iraqi sequence (GenBank)	Reference GenBank accession	Reference isolate origin	Identity (%)	Confirmed species
PX426844.1	MG950136.1	Italy	99	*A. lycopersici*
PX426844.1	KJ729673.1	Netherlands	99	*A. lycopersici*
PX426844.1	MH283415.1	Brazil	98	*A. lycopersici*

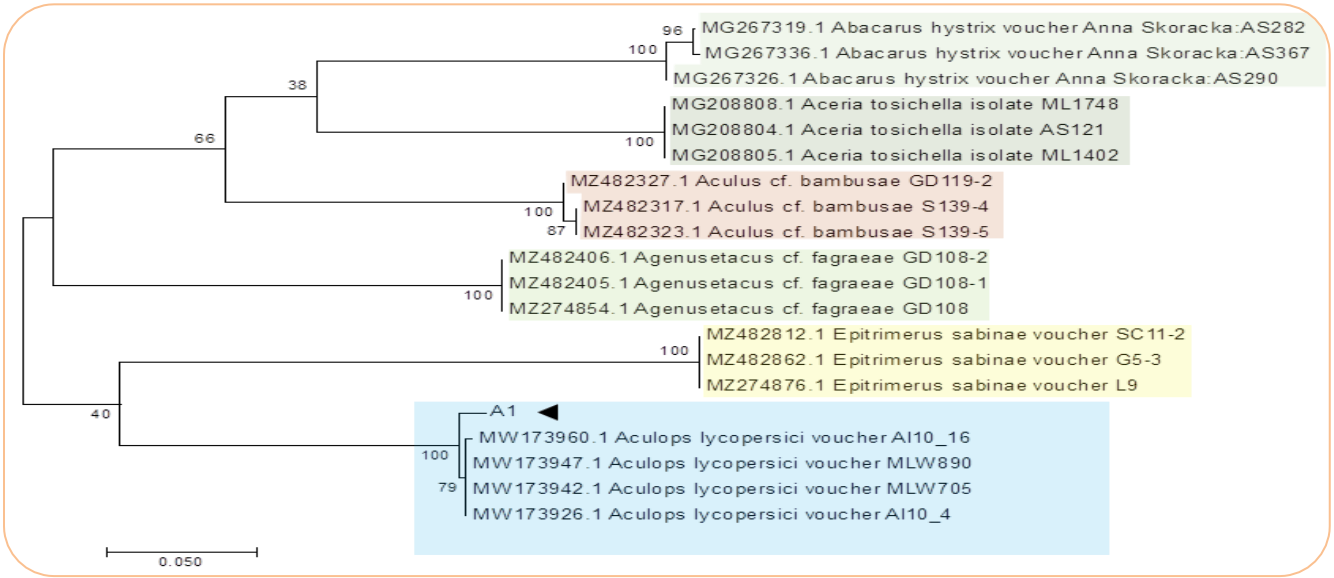


Figure 4. Phylogenetic tree inferred from mitochondrial COI sequences showing the relationship of Iraqi *A. lycopersici* isolates with selected reference sequences from GenBank. An eriophyid species from a related genus was used as an outgroup to root the tree.

The mitochondrial cytochrome c oxidase subunit I (COI) sequence obtained in this study was deposited in the NCBI GenBank database under accession number PX426844.1 (Figure. 5). The sequence is publicly available through the NCBI nucleotide database using the corresponding accession number. https://www.ncbi.nlm.nih.gov/nuccore/PX426844.1.

Conclusions and recommendations

This study constitutes the first formal record of the species, *Aculops lycopersici* (Tryon, 1917), infesting tomato seedlings in central Iraq with molecular confirmation and detailed morphological description. The higher incidence (95.5%) and constant presence of the mite through the growing period indicates that the species is well established in local protected and open-field cultivation systems. Sequences of the mitochondrial COI gene shared high similarity (98-100%) to authenticated international reference sequences, confirming the taxonomic identity of the specimens examined. The phylogenetic analysis also indicated that the Iraqi isolates are members of the world *A. lycopersici* clade. Because of its constant occurrence and potential for causing important foliar damage under favorable environmental conditions, *A. lycopersici* should be regarded as an economically important pest of tomatoes in Iraqi crop production systems. Regular surveying and early detection and incorporation of preventive measures are recommended to avert outbreaks and damage to yield. Population dynamics in varying climates and testing of sustainable control measures in local agricultural settings should be further studied.

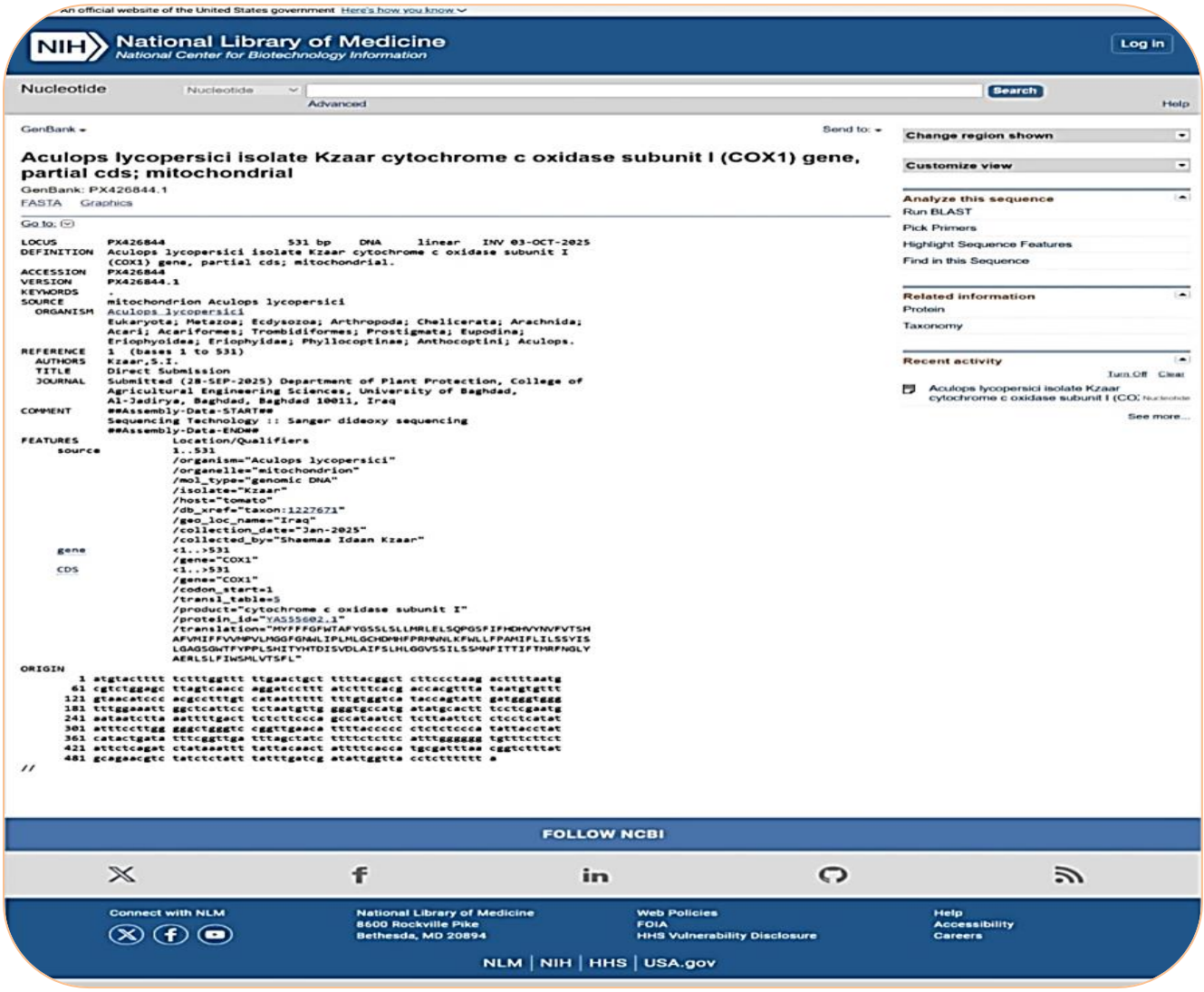


Figure.5. GenBank registration details of *A. lycopersici* COI sequence generated in this study.

Author's contributions

SIK conducted the experiments and drafted the manuscript. HKJA supervised the study and revised the manuscript. Both authors contributed to data analysis and manuscript editing and approved the final version.

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Conflict of Interest

The authors declare no conflict of interest.

Sustainable Development Goals Targeted

SDG 2: Zero Hunger
SDG 12: Responsible Consumption and Production
SDG 15: Life on Land

Policy Addressed

The study was conducted in accordance with international plant health and biosafety guidelines, including IPPC standards for pest identification and FAO frameworks for pest surveillance and IPM. Molecular analyses and genetic data handling complied with CBD and Nagoya Protocol principles, while national regulations of the Iraqi Ministry of Agriculture and Ministry of Environment were followed.

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